EMORY UNIVERSITY DEPARTMENT OF ANTHROPOLOGY

February 18 ANT 206

BRIDGET ALGEE-HEWITT

4:00

A Computational Framework for Estimating Ancestry from Craniometrics: Implications for the Study of Population History and Forensic Identification.

Ancestry is among the most critical, while also among the most challenging, of the biological parameters subject to estimation from the human skeleton. Both methodological and philosophical problems arise from its easy elision with race, ethnicity, and other social identity categories, and the hard-classification approach to its determination using cranial measurements. In this talk, Dr. Algee-Hewitt presents a novel computational framework for ancestry estimation from the cranium that expands the way it is typically conceptualized and treated statistically in biological anthropology. She argues that, in adopting a probabilistic, admixture-driven approach, it is possible to produce more mathematically satisfying and biologically meaningful results, with which we can speak to population dynamics, including, geographic, temporal, and sociocultural trends, draw comparisons between skeletal and genetic-derived patterns, and better attend to social justice concerns in forensic identification contexts.



Bridget F.B. Algee-Hewitt is the Senior Research Scientist and Program Director for the Center for Comparative Studies of Race and Ethnicity at Stanford University. She completed her graduate work in Classical and Near Eastern Archaeology at Bryn Mawr College and in Biological Anthropology at the University of Tennessee – Knoxville. She was the inaugural Haslam post-doctoral fellow for research in forensic sciences at the Forensic Anthropology Center at UT – Knoxville, where she was jointly appointed in the skeletal identification and degraded DNA labs. She was also a post-doctoral fellow in population genetics and computational biology at Stanford University, where she was dual appointed as the Special Scientific Fellow in the Stanford Center for Computational, Evolutionary and Human Genomics.